

P 5 10:01:16 2002

us-09-052-089a-5.rsp

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: September 4, 2002, 16:16:07 ; Search time 172.18 Seconds
(without alignments)
51.241 Million cell updates/sec

Title: US-09-052-089a-5
Perfect score: 1 RALCTICSDPFDHSDVAAM.....IOSFETAPSRTPCPCRIQVG 51
Sequence:

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriaph:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	275	96.2	469	4	000467
2	268	93.7	223	11	Q922M8
3	268	93.7	469	4	Q9BWF2
4	268	93.7	470	11	Q9CP4
5	260	90.9	433	13	Q08854
6	225	78.7	433	13	Q9YGN2
7	114	39.9	310	10	Q82372
8	114	39.9	420	4	Q75866
9	114	39.9	420	4	Q95885
10	114	39.9	455	5	Q9Y8D7
11	113	39.5	158	5	Q9X2S4
12	112	39.2	325	10	Q9M908
13	109.5	38.3	263	5	Q95R85
14	107	37.4	304	5	Q9N3D1
15	106	37.1	349	10	Q947X9
16	103	36.0	344	10	Q65594

17	103	36.0	386	10	Q9L7I4	Q9L7I4 arabidopsis
18	102	35.7	324	10	Q82239	Q82239 arabidopsis
19	102	35.7	327	11	Q9DAH2	Q9DAH2 mus musculu
20	101	35.3	274	10	Q9L210	Q9L210 arabidopsis
21	100	35.0	224	10	Q9M907	Q9M907 arabidopsis
22	100	35.0	285	10	Q9ZTM6	Q9ZTM6 petunia hyb
23	99	34.6	524	10	Q9MA11	Q9MA11 arabidopsis
24	99	34.6	1181	5	Q97260	Q97260 plasmodium
25	98	34.3	325	10	Q9L7U8	Q9L7U8 arabidopsis
26	98	34.3	368	10	Q944L9	Q944L9 arabidopsis
27	98	34.3	383	10	Q9LMT3	Q9LMT3 arabidopsis
28	98	34.3	396	10	Q9FM98	Q9FM98 arabidopsis
29	98	34.3	621	5	Q9V9T8	Q9V9T8 drosophila
30	98	34.3	626	5	Q95SP2	Q95SP2 drosophila
31	97	33.9	291	10	Q9FP62	Q9FP62 mus musculu
32	96.5	33.7	243	11	Q99P05	Q99P05 oryza sativ
33	96.5	33.6	439	10	Q9AGM2	Q9AGM2 arena fatua
34	95.5	33.4	442	10	Q9MAC5	Q9MAC5 homo sapien
35	95.5	33.4	504	4	Q9P04	Q9P04 arabidopsis
36	95.5	33.4	506	10	Q9M143	Q9M143 arabidopsis
37	95	33.2	351	10	Q9ZV08	Q9ZV08 homo sapien
38	94	32.6	137	4	Q9NSR1	Q9NSR1 homo sapien
39	94	32.6	299	10	Q942E6	Q942E6 oryza sativ
40	94	32.9	879	13	Q90ZT8	Q90ZT8 gallus gall
41	94	32.9	923	11	Q90ZT7	Q90ZT7 xenopus lae
42	94	32.9	989	11	Q99ML9	Q99ML9 mus musculu
43	93	32.5	230	10	Q9FN35	Q9FN35 arabidopsis
44	93	32.5	551	3	Q08109	Q08109 saccharomyc
45	92.5	32.3	408	5	Q01482	Q01482 caenorhabdit

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	469 AA.
ID 000467			
AC 000467			
DT 01-JUL-1997 (TREMBLrel. 04, Created)			
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE HTRIP.			
GN Homo sapiens (Human).			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX NCBI_Taxid=9606;			
RN [1]			
RP MEDLINE=97258620; PubMed=9104814;			
RX Lee S.Y., Lee S.Y., Choi Y.;			
RT "TRAF-Interacting protein (TRIP): a novel component of the tumor			
RT necrosis factor receptor (TNFR) - and CD30-TRAF signaling complexes			
RT that inhibits TNFalpha-mediated NF-kappaB activation.";			
RT J. Exp. Med. 185:1275-1285(1997).			
CL -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
CC EMBL: U77845; AAB82993.1; -			
DR InterPro: IPR001841; Znf_Fing.			
DR Pfam: PF00097; zf-C3HC4; 1.			
DR SMART: SM00184; RING; 1.			
DR ZINC-Finger.			
SO SEQUENCE	469 AA;	53138 MW;	2D54ED04B84BAE4 CRC64;

Query Match 96.2%; Score 275; DB 4; Length 469;
Best Local Similarity 96.1%; Pred. No. 1.2e-29;
Matches 49; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RALCTICSDPFDHSDVAAMCGHTFHQCLIOSFETAPSRTPCPCRIQVG 51
DB 4 RALCTICSDPFDHSDVAAMHGGHTFHQCLIOSFETAPSRTPCPCRIQVG 54

DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 470 AA; 53191 MW; 00FD05B52645133 CRC64;

Query Match
Best Local Similarity 90.9%; Score 260; DB 11; Length 470;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALCTICSDPFDRHSDVAAMDCGHTFHLOCLIOSEFTAPSRTPCQCRIOY 51
Db 5 SLCTICSDPFDRHSDVAAMDCGHTFHLOCLIOSEFTAPSRTPCQCRIOY 54

RESULT 6
QY9GN2 PRELIMINARY; PRT; 433 AA.
AC QY9GN2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN TRAF INTERACTING PROTEIN.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCB1_Taxid=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99148833; PubMed-10025966;
RA Cottage A.J., Clark M., Hawker K., Umrana Y., Wheller D., Bishop M.,
RA Elger G.;
RI "Three receptor genes for plasmalogen related growth factors in the
RI genome of the puffer fish Fugu rubripes.";
RT FEBS Lett. 443:370-374(1999).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AJ010317; CA09084.1;
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;

Query Match
Best Local Similarity 78.7%; Score 225; DB 13; Length 433;
Matches 38; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 RALCTICSDPFDRHSDVAAMDCGHTFHLOCLIOSEFTAPSRTPCQCRIOY 50
Db 4 RAQCTICSDPFDRHSDVAAMDCGHTFHLOCLIOSEFTAPSRTPCQCRIOY 53

RESULT 7
ID 082372 PRELIMINARY; PRT; 310 AA.
AC 082372;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN ATG29840. PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCB1_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;

RX MEDLINE-20083487; PubMed-10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.-J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden K., Umeyan L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC005496; AAC35217.1;
DR HSSP: P28990; 1CHC.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 310 AA; 35390 MW; EEE1401152F5E2C CRC64;

Query Match
Best Local Similarity 39.9%; Score 114; DB 10; Length 310;
Matches 19; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

QY 3 LCTICSDPFDRHSDVAAMDCGHTFHLOCLIOSEFTAPSRTPCQCRIOY 50
Db 260 MCSICLIEFDRHSDVAAMDCGHTFHLOCLIOSEFTAPSRTPCQCRIOY 305

RESULT 8
ID 075866 PRELIMINARY; PRT; 420 AA.
AC 075866;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE R3143.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stiliwgen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garces J.,
RA Dangann L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Atlix C., Andreise T., Trankheim M., Amico-Keller G., Coeffield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 2.5 Mb region in 19p13.3.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC005764; AAC62428.1;
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003137; PA.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF02225; PA; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS0186; EGF_2; UNKNOWN_1.
KW Zinc-finger.
SQ SEQUENCE 420 AA; 45880 MW; 572731A8E8A97FCE CRC64;

Query Match
Best Local Similarity 39.9%; Score 114; DB 4; Length 420;

Best Local Similarity 37.5%; Pred. No. 1,4e-07;
Matches 18; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Oy 3 CTTCSDFPHSRDYAMDCGHTFHLOCLIOSFETAPSRTPCPOCR 50
Db 299 LCAITCDEYBERGDKLITPCSHTHYCKCIDPWFESQAPRRSCPCVKQSY 346

RESULT 9

O95SS5 PRELIMINARY; PRT: 435 AA.
AC O95SS5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GH03577P.
GN CG5140.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Chang M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RA Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: AY060610; AAL28158.1;
DR SMART: SM00184; RING; 1.
KW ZINC-finger.
SQ SEQUENCE 435 AA: 48455 MW: 0BF70AC81DD9416E CRC64:

Query Match 39.9%; Score 114; DB 5; Length 435;
Best Local Similarity 47.7%; Pred. No. 1.5e-07;
Matches 21; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

Oy 4 CTTCSDFPHSRDYAMDCGHTFHLOCLIOSFETAPSRTPCPOCR 47
Db 6 CVICAEILFGQADEVFATVCGHMFHNCINQWLDR--SKTPOCR 47

RESULT 10

O9V8D7 PRELIMINARY; PRT: 455 AA.

AC O9V8D7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CG5140 PROTEIN.
GN CG5140.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MEDLINE=20196006; Pubmed-10731132;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doop L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glusker A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Stong R., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wattarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC 1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL: AED03800; AAF57730.1;
DR FLYbase: FBgn0034314; CG5140.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW ZINC-finger.
SQ SEQUENCE 455 AA: 50726 MW: BEA74FACACE8FD5B CRC64:

Query Match 39.9%; Score 114; DB 5; Length 455;
Best Local Similarity 47.7%; Pred. No. 1.5e-07;
Matches 21; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

Oy 4 CTTCSDFPHSRDYAMDCGHTFHLOCLIOSFETAPSRTPCPOCR 47
Db 6 CVICAEILFGQADEVFATVCGHMFHNCINQWLDR--SKTPOCR 47

RESULT 11

O9XZS4 PRELIMINARY; PRT: 158 AA.

AC O9XZS4;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EG:22E5.12 OR CG4325.
GN EG:22E5.12 OR CG4325.

OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;
RC MEDLINE=20196006; Pubmed-10731132;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Domes K., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durlin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fossil C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Matell B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.Y., Mobarry C., Morris J., Moshireli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Put V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Stykars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL science 287:2185-2195(2000).

RA [2] SEQUENCE FROM N.A.
RA Murphy L., Harris D., Barrell B.;
RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL submitted (sep-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RP Benos P.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AE003422; AAF45708.1; -;
DR EMBL: AL031765; CAB41708.1; -;
DR FLYBASE: FBgn0026878; EG:225.12.
DR InterPro: IPR001841; Znf.fing.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR zinc-finger.
KW SEQUENCE 158 AA; 17741 MW; 21C417B040642D73 CRC64;

Query Match 39.5%; Score 113; DB 5; Length 158;
Best Local Similarity 48.9%; Pred. No. 7.2e-08;
Matches 23; Conservative 4; Mismatches 18; Indels 2; Gaps 1;
OY 3 LCTICSDFFDHSRDV--AAMDGHTFHLOCLIOSEFETAPSTCPQCR 49
Db 7 ICTICSEFRITSDNIOAGSGHAFHEDCL--DHWKQSRTPCICRSQ 51

RESULT 12
ID 09M908 PRELIMINARY; PRT; 325 AA.
AC 09M908;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE F6A14.12 PROTEIN.
GN F6A14.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

RP SEQUENCE FROM N.A.
RA Federpiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Kowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Luvos S., Schwartz J., Shin P., Toriumi M., Vystotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC011809; AAF27102.1; -;
DR InterPro: IPR001664; IF.
DR InterPro: IPR001841; Znf.fing.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00226; IF; UNKNOWN_1.
KW zinc-finger.
KW SEQUENCE 325 AA; 36919 MW; 837FDB7F28F2B615 CRC64;

Query Match 39.2%; Score 112; DB 10; Length 325;
Best Local Similarity 37.5%; Pred. No. 2.1e-07;
Matches 18; Conservative 11; Mismatches 17; Indels 2; Gaps 1;
OY 3 LCTICSDFFDHSRDV--AAMDGHTFHLOCLIOSEFETAPSTCPQCR 50
Db 276 VCTICLEFDDGSRIVTLPCGHEFDECVLEWF--VRSHVCPCLRUEL 321

RESULT 13
ID 095RB5 PRELIMINARY; PRT; 263 AA.
AC 095RB5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE ID46221P.
GN CG10916.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=Y, CN BW SP;
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farlan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY061504; AAL29052.1; -;
DR SEQUENCE 263 AA; 29515 MW; B98CECE994071BFF CRC64;

Query Match 38.3%; Score 109.5; DB 5; Length 263;
Best Local Similarity 46.8%; Pred. No. 3.7e-07;
Matches 22; Conservative 6; Mismatches 14; Indels 5; Gaps 3;
OY 3 LCTICSDFFDHSRDV--AAMDGHTFHLOCLIOSEFETAPSTCPQCR 47
Db 31 LCAICNEFF-RANDITFSTRSGHVFHKDCLTRMLNR--SRTCPQCR 74

RESULT 14
ID 09N3D1 PRELIMINARY; PRT; 304 AA.
AC 09N3D1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
GN y5E10BR.3.
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode *C. elegans*: a platform for
investigating biology. The *C. elegans* Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [12]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Tin-Mollam A., Becker M., Graves T.;
RT "The sequence of *C. elegans* cosmid Y54E10B.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [13]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AC024812; AAF59555.1; -;
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KM Hypothetical protein; Zinc-finger.
SQ SEQUENCE 304 AA; 33447 MW; 3E522361AFA54C44 CRC64;

Query Match 37.4%; Score 107; DB 5; Length 304;
Best Local Similarity 42.9%; Pred. No. 9.4e-07;
Matches 21; Conservative 5; Mismatches 21; Indels 2; Gaps 1;
OY 2 ALCCTCSDFDHSRDVAAADCCTHFLCCLIOSFETAPSRCPQCRIOV 50
DB 236 AACTCTCFDFKLEDEVDGALDCNHFHRCIEPWLKT--KNSCPVCROKV 282
RESULT 15
ID 0947X9 PRELIMINARY; PRT; 349 AA.
AC 0947X9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHEICAL 39.6 KDA PROTEIN.
GN OSJNBA0067N01.18.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-NIPPONBARE;
RA de la Bastide M., Spiegel L., Preston R., Kirchoff K., King L.,
RA Nascimento L., Baker J., Vil M.D., Zulfavert T., Santos L., Miller B.,
RA Kuit K., Cunnius D.M., Rodriguez S., Balija V., Shah R., Bahret A.,
RA Yang C., Bell M., Palmer L., O'Shaughnessy A., Dedha N.,
RA McCumle W.R.;
RT "Genomic Sequence for *Oryza sativa*, Nipponbare strain, clone
OSJNBA0067N01, from chromosome 3, complete sequence.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC090485; AAK98739.1; -;
KM Hypothetical protein.
SQ SEQUENCE 349 AA; 39557 MW; ECF2CDDC80C2E2DE1 CRC64;

Query Match 37.1%; Score 106; DB 10; Length 349;
Best Local Similarity 38.6%; Pred. No. 1.5e-06;

Matches 17; Conservative 12; Mismatches 13; Indels 2; Gaps 2;
OY 4 CTTCSDFFDHSRDVAAADCCTHFLCCLIOSFETAPSRCPQCR 46
DB 212 CPVCFEYLFDSKTRDISALCHGTHLECLYE-MRSHQOFCPCVC 254

RESULT 16
ID 065594 PRELIMINARY; PRT; 344 AA.
AC 065594;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHEICAL 38.7 KDA PROTEIN.
GN M3E9.170 OR AT4G26400.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Bevan M., Vandenberg M., Jallet C., Portetelle D., Hohnsels J.,
RA Mewes H.W., Mayer K., Schueller C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 65-344 FROM N.A.
RA rose M., Hempel S., Eutlian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Vandenberg M., Jallet C., Portetelle D., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AL016165; CAB79495.1; -;
DR EMBL; AL161565; CAB79495.1; -;
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KM Hypothetical protein; Zinc-finger.
SQ SEQUENCE 344 AA; 36720 MW; EB31D0BF5EDA700 CRC64;

Query Match 36.0%; Score 103; DB 10; Length 344;
Best Local Similarity 38.3%; Pred. No. 3.8e-06;
Matches 18; Conservative 8; Mismatches 19; Indels 2; Gaps 1;
OY 4 CTTCSDFFDHSRDVAAADCCTHFLCCLIOSFETAPSRCPQCRIOV 50
DB 229 CSTCLDDPDKGSEAKEMPCRKHFHRCIVPWLHSS--CPVCYVEL 273

RESULT 17
ID 09LT14 PRELIMINARY; PRT; 386 AA.
AC 09LT14;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 3, PL CLONE: MPV9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.

Query Match	35.7%	Score 102	DB 10	Length 324
Best Local Similarity	41.3%	Pred. No. 4.9e-06		
Matches 19	Conservative 6	Mismatches 19	Indels 2	Gaps 1
Oy	4	CTIC--SDPFHSDRVAAADCGHTFHLOCLIOSFETAPSRTPCPCR	47	
Db	38	CSICLESYLDDEGRSKAKLCGCHPHLOLCIGSAFMNKGAMGCPNCR	83	
RESULT	19			
O9DAH2				
ID	O9DAH2	PRELIMINARY:	PRT:	327 AA.
AC	O9DAH2:			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	SPERMATID SPECIFIC RING ZINC FINGER 1.			
CS	SSRZFL			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=TESTIS;			
RC	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,			
RA	Atawa K., Iwawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., Rong B., Kochiya H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schiraldi L., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontuski S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
CC	-I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	HSP: AK005843; BAB24269.1; -			
DR	HSP: P28990; ICHC.			
DR	MGD: MGI:1341258; Ssrzfl.			
DR	InterPro: IPR000561; EGF-like.			
DR	InterPro: IPR001841; Znf_ring.			
DR	Pfam: PF00097; zf-C3HC4; 1.			
DR	SMART: SM00184; RING: 1.			
DR	PROSITE: PS01186; BGF_2; UNKNOWN_1.			
DR	Zinc-finger.			
KW	SEQUENCE 327 AA; 35627 MW; 5F8D34ABEE394193 CRC64;			
Query Match	35.7%	Score 102	DB 11	Length 327
Best Local Similarity	33.3%	Pred. No. 4.9e-06		
Matches 16	Conservative 9	Mismatches 23	Indels 0	Gaps 0
Oy	3	LCITCSDFHSDRVAAADCGHTFHLOCLIOSFETAPSRTPCPCR	50	
Db	208	LCATCIDLDYEEGERLKILPCAHAYHCRCIDPWFSAARSSCPLKROSV	255	
RESULT	20			
O9LZ10				
ID	O9LZ10	PRELIMINARY:	PRT:	274 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEtical 31.1 KDA PROTEIN.
GN F6G14_60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RA Bevan M., Terryn N., Ardiles W., Buyschaert C., Dasseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielens J., Van Montagu M., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AL162973; CAB66029.1; -;
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KW Hypothetical protein; zinc-finger.
SQ SEQUENCE 274 AA; 31102 MW; 9A98B6C495A6F068 CRC64;

Query Match 35.3%; Score 101; DB 10; Length 274;
Best Local Similarity 38.3%; Pred. No. 5; 6e-06;
Matches 18; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 4 CTICSEFDHSRDVAMDCGHTFHLOCLIOSFETAPSRTPCPCQIQV 50
DB 205 CVYCEEMSEGRDVCPCMHFFHMKCLPWL--SKNMCPCPCRFGL 249

RESULT 21
ID 09M9U7 PRELIMINARY; PRT; 224 AA.
AC 09M9U7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F6A14.13 PROTEIN.
GN F6A14.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altati H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremetska I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shin P., Toriumi M., Vysotskaya V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AC01809; AAF27103.1; -;
DR HSSP; P28990; ICHC.
DR InterPro; IPR003903; UIM.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 224 AA; 26040 MW; 563926B745C61F8C CRC64;

Query Match 35.0%; Score 100; DB 10; Length 224;

Best Local Similarity 38.3%; Pred. No. 6; 3e-06;
Matches 18; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

QY 4 CTICSEFDHSRDVAMDCGHTFHLOCLIOSFETAPSRTPCPCQIQV 50
DB 175 CTICLEFNDGTRVWTLPCGHEFDECVLTFET--NHDCPLCRFKL 219

RESULT 22
ID 09ZTM6 PRELIMINARY; PRT; 285 AA.
AC 09ZTM6;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PGPD14.
GN PGPD14.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN
RP SEQUENCE FROM N.A.
RA TISSUE-GERMINATING PETUNIA POLLEN TREATED WITH KAEPPEROL;
RX MEDLINE=20317212; PubMed=10859200;
RA Guyon V.N., Astwood J.D., Garner E.C., Dunker A.K., Taylor L.P.;
RT "Isolation and characterization of cDNAs expressed in the early stages
of flavonol-induced pollen germination in petunia.";
RL Plant Physiol. 123:699-710(2000).
DR EMBL; AF049930; AAD02556.1; -;
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING; 1.
KW SMART; SM00184; RING; 1.
SQ SEQUENCE 285 AA; 32987 MW; BAD20BC86F1D3D86 CRC64;

Query Match 35.0%; Score 100; DB 10; Length 285;
Best Local Similarity 36.4%; Pred. No. 8e-06;
Matches 16; Conservative 12; Mismatches 14; Indels 2; Gaps 2;

QY 4 CTICSEFDHSRDVAMDCGHTFHLOCLIOSFETAPSRTPCPCQ 46
DB 162 CPVCFEYFDTKNTIVLPCGHTMLECVWQ--MEQINQISCPVC 204

RESULT 23
ID 09MA11 PRELIMINARY; PRT; 524 AA.
AC 09MA11;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F12M16.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RA Kim C., Brooks S., Buehler E., Chao O., Dunn P., Khan S., Shin P.,
RA Altati H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
RA Huizar L., Kremetska I., Lenz C., Li J., Liu S., Luros S.,
RA Huizar L., Schwartz J., Toriumi M., Vysotskaya V., Yu G., Davis R.W.,
RA Federspiel N.A., Theologis A., Ecker J.R.;
RL "Genomic sequence for Arabidopsis thaliana BAC F12M16 from chromosome
1.";
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AC008007; AAF69531.1; -;
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.

KW Zinc-finger.
SQ SEQUENCE 524 AA; 58471 MW; CFC6AB4E39BD6FF CRC64;

Query Match 34.6%; Score 99; DB 10; Length 524;
Best Local Similarity 36.4%; Pred. No. 2e-05;
Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFLQCLIOSEFTAPSRTPCQCR 47
DB 472 CTICSESKNEKATATDCGHEHYAECLERKL--IVANVCPICK 513

RESULT 24

O97260 PRELIMINARY; PRT; 1181 AA.

AC O97260; (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOHETICAL 135.6 KDA PROTEIN.
GN PRC0610C, MAL3P5.8
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_Taxid=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Felwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrett B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum.";
RL Nature 400:532-538(1999).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AL034556; CAB8971.1; -.
DR HSSP: P28990; ICHC.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KM Hypothetical protein; Zinc-finger.
SQ SEQUENCE 1181 AA; 135638 MW; 288C44EAFB8C2D4 CRC64;

Query Match 34.6%; Score 99; DB 5; Length 1181;
Best Local Similarity 34.0%; Pred. No. 4.7e-05;
Matches 16; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFLQCLIOSEFTAPSRTPCQCR 50
DB 1131 CCICCEYQNDVNIPLCTHNFHKQCLIKWI--SKNTCPCLXIDL 1175

RESULT 25

O9LTU8 PRELIMINARY; PRT; 325 AA.

AC O9LTU8; (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GB|AA27103.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC

RT clones.";
RL DNA Res. 7:131-135(2000).

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL: AB024034; BAB02789.1; -.
DR HSSP: P28990; ICHC.

DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00184; RING; 1.
KM Zinc-finger.
SQ SEQUENCE 325 AA; 36432 MW; 694044F361053DE4 CRC64;

Query Match 34.3%; Score 98; DB 10; Length 325;
Best Local Similarity 38.3%; Pred. No. 1.7e-05;
Matches 18; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFLQCLIOSEFTAPSRTPCQCR 50
DB 275 CTICLEFNFAGGILVALPCGHDFDECAVWFET--NHFCPLCYREL 319

RESULT 26

O944L9 PRELIMINARY; PRT; 368 AA.

AC O944L9; (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ATG1970/F2H15.16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carlincl P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yanada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF428290; AL16122.1; -.
SQ SEQUENCE 368 AA; 41618 MW; 79AD48BD0790A08E CRC64;

Query Match 34.3%; Score 98; DB 10; Length 368;
Best Local Similarity 34.1%; Pred. No. 2e-05;
Matches 15; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFLQCLIOSEFTAPSRTPCQCR 47
DB 320 CSICDEYERDEDEVELNGSHFVHCVKWLL--SRKNACPVCK 361

RESULT 27

O9LMT3 PRELIMINARY; PRT; 363 AA.

AC O9LMT3;
ID O9LMT3;
RN [1]
RP SEQUENCE FROM N.A.

DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE F2H15.19 PROTEIN.
GN F2H15.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sakano H., Liu S.X., Eguu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
RA Alcafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
RA Nguyen M., Palm C.J., Shin P., Southwick A., Davis R.W., Ecker J.R.,
RA Federspiel N.A., Theologis A.;
RT "The sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC034106; AAF97276.1; -;
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger
SQ SEQUENCE 363 AA: 43262 MW: 884DEBE9FE0B224 CRC64;

Query Match 34.3%; Score 98; DB 10; Length 383;
Best Local Similarity 34.1%; Pred. No. 2e-05;
Matches 15; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

OY 4 CTGCSDFDHSRDVAMDCGHTFHLCQIOSFETAPSTPCQCR 47
Db 335 CSICDYEYREDEYELNGSHFHVCKVQWL--SRKNACPVCK 376

RESULT 28
O9FW98 PRELIMINARY; PRT; 396 AA.
AC O9FW98;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 5, PL CLONE:MCD.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Physically assigned pl and rnc clones.";
RL DNA Res. 5:41-54(1998).
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AB009049; BAB11261.1; -;
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger
SQ SEQUENCE 396 AA: 44359 MW: 43059E73B4442FFB CRC64;

Query Match 34.3%; Score 98; DB 10; Length 396;
Best Local Similarity 34.0%; Pred. No. 2.1e-05;

Matches 16; Conservative 10; Mismatches 19; Indels 2; Gaps 1;
OY 4 CTGCSDFDHSRDVAMDCGHTFHLCQIOSFETAPSTPCQCR 50
Db 259 CSVCIDPEKCTEAKEMPCRKHFVRCIVPMLTELHSS--CVCRRFL 303

RESULT 29
O9V978 PRELIMINARY; PRT; 621 AA.
AC O9V978;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CG1937 PROTEIN.
GN CG1937.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sultón G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaskey E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burris R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jbalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AE003779; AAF57196.1; -;
DR FlyBase: FBgn0039875; CG1937.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger
SQ SEQUENCE 621 AA: 68752 MW: A8D6EB1609E2C0A1 CRC64;

Query Match 34.3%; Score 98; DB 5; Length 621;
Best Local Similarity 38.8%; Pred. No. 3.3e-05;
Matches 19; Conservative 8; Mismatches 16; Indels 6; Gaps 3;
OY 3 LCTIC-SDPFDHSDVAMDCGHTFHLOCLIOSEFTAPSRQCRCQOV 50
DB 279 ICITICREDMNVNHSK---KLPCGHIFHTTCLRSWFOR--QQTCTPCRLNI 322

RESULT 30
O95SP2 PRELIMINARY; PRT; 626 AA.
AC O95SP2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE GH1111P.
GN CG1937.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY060677; AAL28225.1; - F81B88D51D724EC CRC64;
SQ SEQUENCE 626 AA; 69272 MW; F81B88D51D724EC CRC64;

Query Match 34.3%; Score 98; DB 5; Length 626;
Best Local Similarity 38.8%; Pred. No. 3.4e-05;
Matches 19; Conservative 8; Mismatches 16; Indels 6; Gaps 3;
OY 3 LCTIC-SDPFDHSDVAMDCGHTFHLOCLIOSEFTAPSRQCRCQOV 50
DB 288 ICITICREDMNVNHSK---KLPCGHIFHTTCLRSWFOR--QQTCTPCRLNI 331

RESULT 31
O95FB6 PRELIMINARY; PRT; 291 AA.
AC O95FB6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PGPD14 PROTEIN (AT5G22920/MRN17.15).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA.
RA MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones."
RL DNA Res. 4:215-230(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AB005243; BAB10613.1; -
DR EMBL: AY052362; AAK96553.1; -
DR InterPro: IPR000345; CYTC_heme_bind.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Zinc-finger.
SQ SEQUENCE 291 AA; 33549 MW; A54E62844ED93A66 CRC64;

Query Match 33.9%; Score 97; DB 10; Length 291;
Best Local Similarity 38.6%; Pred. No. 2.1e-05;
Matches 17; Conservative 8; Mismatches 17; Indels 2; Gaps 2;
OY 4 CTICSDP-FDHSRDVAMDCGHTFHLOCLIOSEFTAPSRQCRCQ 46
DB 163 CPVCFEYLFSDTRDITVRCGHTMHLCC-TKDMGLHNRITCPVC 205

RESULT 32
O99PO5 PRELIMINARY; PRT; 243 AA.
AC O99PO5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TRIPARTITE MOTIF PROTEIN TRIM7.
GN TRIM7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231161; PubMed=11331580;
RA Raymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L.,
RA Riganello D., Zanaria E., Messali S., Calinara S., Guiffanti A.,
RA Minucci S., Pellici P.G., Balabio A.;
RT "The tripartite motif family identifies cell compartments."
RL EMBL J. 20:2140-2151(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF220033; AAG53487.1; -
DR HSSP: P15919; IRMD.
DR MGD: MGI:2137353; Trim7.
DR InterPro: IPR000315; ZnF_box.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00643; zf-B_box; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 243 AA; 27256 MW; 284F3D48E8EBC781 CRC64;

Query Match 33.7%; Score 96.5; DB 11; Length 243;
Best Local Similarity 32.8%; Pred. No. 2.1e-05;
Matches 19; Conservative 12; Mismatches 12; Indels 15; Gaps 2;
OY 2 ALCTICSDPFDHSDVAMDCGHTFHLOCLIOSEFTAPSRQCRCQ 47
DB 27 ATCTICLERF---REPVSVECHSFCRACIMKWERPAGTGTATRTLPCLPCPCR 81

Query Match	33.4%	Score 95.5;	DB 10;	Length 506;
Best Local Similarity	39.6%	Pred. No. 6e-05;		
Matches	21; Conservative	0; Mismatchal		

RESULT 37

01-MAY-1999 (TREMblrel. 10, Created)
01-DEC-2001 (TREMblrel. 10, Last sequence update)
T5A14.7 PROTEIN (AT1655530/T5A14.7, Last annotation update)

Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta, eudicotyledons, core eudicots, Rosidae eucosids II: Brassicales, Brassicaceae: Arabidopsis.
NCBI_TaxID=3702.

SEQUENCE FROM N.A.
Pederspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Alfitti H., Arzujo R., Huizar L., Rowley D., Beukler E., Dunn P.,
Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
Walker M., Yu G.Ecker J., Theologos A., Davis R.W.;
Submitted (Jan-1999) to the EMBL/GenBank/DBJ databases.
[12]

Cheek R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bower L., Canicini P., Dale J.M., Goldsmith A.D., Hayasizaki Y., Ishida J., Jiang P.X., Jones T., Kanlaya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakuraba S., Satou M., Seiki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[3]

SEQUENCE FROM N.A.
Shlin P., Chen H., Cheuk R., Kim C. J., Koeseema E., Meyers M.C.,
Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A.,
Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P. X., Jones T.,
Kamya A., Karlin-Neumann G., Kawal J., Lam B., Lee J.M., Lin J.,
Liu S.X., Miranda M., Natsumaka M., Nguyen M., Onodera C.S., Palm C.,
Pham P.K., Quach H.L., Sekurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriuni M., Yamada K., Yu G., Yu S., Shinozaki K.,
Davis R.W., Theologis A., Ecker J.R.,
"Arabidopsis cDNA clones."
Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
- i- Similarity: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL: AC005223; AAD10644.1; -
EMBL: AF428378; AAL1572.1; -
EMBL: AY039608; AAK62663.1; -
InterPro: IPR001841; Znf_fing.
Pfam: PF00097; zf-CHC4_1.
SMART: SM00184; RING; 1.
Zinc-finger.

SEQUENCE 351 AA; 38963 MW; DE5ABB4D72CF7075 CRC64;

223 CSYCLDDEFGTEAKLMCTHKHSDCLLFWLEHSS--CPVCRQL 267

SULT 38
NSRI
Q9NSRI
Q9NSRI;
PRELIMINARY;
PRT; 137 AA.

01-OCT-2000 (TREMBLrel, 15, Created)
01-OCT-2000 (TREMBLrel, 15, Last sequence update)
01-DEC-2001 (TREMBLrel, 19, Last annotation update)
HYPOHETICAL15.7 KDA PROTEIN (LIKELY ORTHOLOG OF MOUSE ARRADIA)
DKEFZ761D081.

homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

[1] SEQUENCE FROM N.A.
TISSUE-AMYGALA;
Olttenweelder B., Obermaier B., Mewes H.W., Weill B., Wiemann S.:
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]

SEQUENCE FROM N.A. TISSUE-BRAIN, PRIMITIVE NEUROECTODERMAL; Strausberg R.; Submitted (Jun-2001) to the EMBL/GenBank/DBD databases
- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL: AI157444 CDS147

EMBL: BC010369; AAH10369.1; -
InterPro: IPR001841; Znf_ring.
Pfam: PF00097; zf-C3HC4; 1.

SMART; SM00184; RING; 1.
Hypothetical protein; zinc-finger.
SEQUENCE 137 AA; 15739 MW; 6AA62DC6CEE8C114 CRC64;

Very March	32.98;	Score 94;	DB 4;	Length 137;
1st Local Similarity	36.28;	Pred. No.	2.5e-05;	
17.5-20.0				

	1; conservative	7; mismatches	21; indels	2; gaps	1;
4	CTICSDPFDHSRDVAAMDCGTTFLCLOISQSFETASRCPQCRQV				50
		:			
		:			
		:			
85	CTICSLIIEEGEDVRLPLCMHLFHCYCVQDMILT--NKKPCICRVDI				129

LT 39
E6
Q942E6 PRELIMINARY;
Q942E6. PRT; 299 AA

01-DEC-2001 (Tremblrel. 19, Created)
01-DEC-2001 (Tremblrel. 19, last sequence update)
01-DEC-2001 (Tremblrel. 19, last annotation update)
PUTATIVE PGED14 PROTEIN (POLLEN GERMINATION RELATED PROTEIN),
0408C01.20.

Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
NCBI_TaxID=4530;

SEQUENCE FROM N.A.
STRAIN=CV. NIPPOBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare (GA3) genomic
clone: F0480c01" DNA, chromosome 1, PAC

